

SEQUENCE LISTING

<110> Boyle, Bryan J
 Yeung, George
 Mize, Nancy K
 Arterburn, Matthew C
 Tang, Y. Tom
 Liu, Chenghua
 Drmanac, Radoje T
 Wang, Menq-Yun
 Chen, Lichuan
 Yang, Yea-Huey

<120> METHODS AND MATERIALS RELATING TO LEUCINE-RICH REPEAT PROTEIN-LIKE (LRR PROTEIN-LIKE) POLYPEPTIDES AND POLYNUCLEOTIDES

<130> HYS-26

<140> NOT YET ASIGNED

<141> 2000-09-27

<150> US 09/560,875

<151> 2000-04-27

<150> US 09/496,914

<151> 2000-02-03

<160> 22

<170> PatentIn version 3.0

<210> 1

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(477)

<223> n = A, T, G or C

<400> 1
 ttcccggggc gacgatttcg tgtccctggc ggngaacacc atcatgcggc tggacgactc 60
 cgtcttcgat ggcttgagc gtctccggga gctggatctg cagaggaact acatcttcga 120
 gatcgagggc ggcgcttttcg acggcctggc tgagctgagg cacctcaacc tggccttcaa 180
 caacctcccc tgcacgtggtg acttcgggct cagcgggctg cgggtcctca acgtcagcta 240
 caacgtcctg gagtggttcc tcgcgaccgg gggagaggct gccttcgagc tggagacgct 300
 ggacctgtct cacaaccagc tgctgttctt cccgctgctg cccagtaga gcaagttgctg 360
 gacctcctg ctgcgcgaca acaacatggg cttctaccgg gacctgtaca acacctcgctc 420
 gccgagggag atggtggccc agttcctcct cgtggacggc aacgtgacca acatcan 477

<210> 2
 <211> 1411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1411)
 <223> n = A, T, G or C

<400> 2
 caaaaggac aaagtggtt gtccatgcaa ccgtttaag acccgcgga atcactacct 60
 aaagccttac cctataatgg agagaatcag cctgcccagc tgccacgtag agagcatcat 120
 ccgcgcgcc ttccaggagc aaggtcacct gcgcagcttg gacggggggg tcacatgcct 180
 ctcagagagc tccgaataga cgcgcaaccg ccctccacgc cctgccgggc ctgcggaggc 240
 tggacttgctc aggaacgcc ctgacggagg acatggcagc cctcatgctc cagaacctct 300
 cctcgctgcg gtccgtgtcc ctggcgggga acaccatcat gcggctggac gactccgtct 360
 ttcgagggcc tggagcgtct ccgggagctg gatcttgag aggaactaca tcttcgagat 420
 cgagggcggc gcttttcgac ggcctgggct tgagctgagg cacctcaacc tgggcctttc 480
 aacaacctcc cctgcatcgt ggacttcggg ctacgcggc tgcgggtcct caacgtcagc 540
 cacaacgtcc tggagtgggt cctcgcgacc gggggagagg ctgccttcga gctggtgagc 600
 tctgtctctg tctcacaatc agttagcggg tcttcccgtc gctgccccag tacagcaagt 660
 tggggaccct cctgctgcgc gagaacaaca tgtgcttcta ccgggacctg tacaacacct 720
 cgtcgcgag ggagatgggt gccagttcc tctcgtgga cggcaacgtg accaaccatca 780
 ccaccgtcag cctctgggaa gaattctcct ccagcgacct cgcagatctc cgcttctctg 840
 acatgagcca gaaccagttc cagtacctgc cagacggctt cctgaggaaa atgccttccc 900
 tctccacct gaacctccac cagaattgcc tgatgacgct tcacattcgg gagcacgagc 960
 cccccggagc gctcaccgag ctggacctga gccacaacca gctgtcggag ctgcacctgg 1020
 ctccggggct ggccagctgc ctgggcacgc tgcgcttggt caacctgagc tccaaccagc 1080
 tctggggcgt cccccctggc ctcttcgcca atgctaggaa catcactaca cttgacatga 1140
 gccacaatca gatctcactt tgtcccctgc cagctgcctc ggaccgggtg ggcccccta 1200
 gctgtgtgga ttccaggaat atggcatctt taaggagcct gtctctggag ggctgggcct 1260
 gggggcatta ccgactgcc attccaaggg acctccctga ctacttagac tctcaagcac 1320
 tggggggctc gaaaggagc ctcgcccact ccaagatgtg ccccatgtac agggctgttt 1380
 ctttaggaca tnggctcact cagcttatgc c 1411

004260-1-092700

<210> 3
 <211> 2438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (168)..(2246)

<400> 3
 gtgacttcag tttccgtccg ttccttccgc tgggtgctaaa ataatctgat gccccacagc 60
 aaggaggtag cccagccccg cgttcggctg ctctcgagga ggccggagcc cccggagacg 120
 atgcgccccg cgagccgcct gcgcctgcgg gagcggctgc ccttgat atg gag ttg 176
 Met Glu Leu
 1
 ctg cct ctt tgg ctc tgc ctg ggt ttt cac ttc ctg acc gtg ggc tgg 224
 Leu Pro Leu Trp Leu Cys Leu Gly Phe His Phe Leu Thr Val Gly Trp
 5 10 15
 agg aac aga agc gga aca gcc aca gca gcc tcc caa gga gtc tgc aag 272
 Arg Asn Arg Ser Gly Thr Ala Thr Ala Ala Ser Gln Gly Val Cys Lys
 20 25 30 35
 ttg gtg ggt gga gcc gct gac tgc cga ggg cag agc ctc gct tgc gtg 320
 Leu Val Gly Gly Ala Ala Asp Cys Arg Gly Gln Ser Leu Ala Ser Val
 40 45 50
 ccc agc agc ctc ccg ccc cac gcc cgg atg ctc acc ctg gat gcc aac 368
 Pro Ser Ser Leu Pro Pro His Ala Arg Met Leu Thr Leu Asp Ala Asn
 55 60 65
 cct ctc aag acc ctg tgg aat cac tcc ctc cag cct tac cct ctc ctg 416
 Pro Leu Lys Thr Leu Trp Asn His Ser Leu Gln Pro Tyr Pro Leu Leu
 70 75 80
 gag agc ctc agc ctg cac agc tgc cac ctg gag cgc atc agc cgc ggc 464
 Glu Ser Leu Ser Leu His Ser Cys His Leu Glu Arg Ile Ser Arg Gly
 85 90 95
 gcc ttc cag gag caa ggt cac ctg cgc agc ctg gtc ctg ggg gac aac 512
 Ala Phe Gln Glu Gln Gly His Leu Arg Ser Leu Val Leu Gly Asp Asn
 100 105 110 115
 tgc ctc tca gag aac tac gaa gag acg gca gcc gcc ctc cac gcc ctg 560
 Cys Leu Ser Glu Asn Tyr Glu Glu Thr Ala Ala Ala Leu His Ala Leu
 120 125 130
 ccg ggc ctg cgg agg ctg gac ttg tca gga aac gcc ctg acg gag gac 608
 Pro Gly Leu Arg Arg Leu Asp Leu Ser Gly Asn Ala Leu Thr Glu Asp
 135 140 145
 atg gca gcg ctc atg ctc cag aac ctc tcc tgc ctg cgg tcc gtg tcc 656
 Met Ala Ala Leu Met Leu Gln Asn Leu Ser Ser Leu Arg Ser Val Ser
 150 155 160
 ctg gcg ggg aac acc atc atg cgg ctg gac gac tcc gtc ttc gag ggc 704

004260 "T221" 092700

Leu Ala Gly Asn Thr Ile Met Arg Leu Asp Asp Ser Val Phe Glu Gly	
165 170 175	
ctg gag cgt ctc cgg gag ctg gat ctg cag agg aac tac atc ttc gag	752
Leu Glu Arg Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr Ile Phe Glu	
180 185 190 195	
atc gag ggc ggc gct ttc gac ggc ctg gct gag ctg agg cac ctc aac	800
Ile Glu Gly Gly Ala Phe Asp Gly Leu Ala Glu Leu Arg His Leu Asn	
200 205 210	
ctg gcc ttc aac aac ctc ccc tgc atc gtg gac ttc ggg ctc acg cgg	848
Leu Ala Phe Asn Asn Leu Pro Cys Ile Val Asp Phe Gly Leu Thr Arg	
215 220 225	
ctg cgg gtc ctc aac gtc agc tac aac gtc ctg gag tgg ttc ctc gcg	896
Leu Arg Val Leu Asn Val Ser Tyr Asn Val Leu Glu Trp Phe Leu Ala	
230 235 240	
acc ggg gga gag gct gcc ttc gag ctg gag acg ctg gac ctg tct cac	944
Thr Gly Gly Glu Ala Ala Phe Glu Leu Glu Thr Leu Asp Leu Ser His	
245 250 255	
aac cag ctg ctg ttc ttc ccg ctg ctg ccc cag tac agc aag ttg cgg	992
Asn Gln Leu Leu Phe Phe Pro Leu Leu Pro Gln Tyr Ser Lys Leu Arg	
260 265 270 275	
acc ctc ctg ctg cgc gac aac aac atg ggc ttc tac cgg gac ctg tac	1040
Thr Leu Leu Leu Arg Asp Asn Asn Met Gly Phe Tyr Arg Asp Leu Tyr	
280 285 290	
aac acc tcg tcg ccg agg gag atg gtg gcc cag ttc ctc ctc gtg gac	1088
Asn Thr Ser Ser Pro Arg Glu Met Val Ala Gln Phe Leu Leu Val Asp	
295 300 305	
ggc aac gtg acc aac atc acc acc gtc agc ctc tgg gaa gaa ttc tcc	1136
Gly Asn Val Thr Asn Ile Thr Thr Val Ser Leu Trp Glu Glu Phe Ser	
310 315 320	
tcc agc gac ctc gca gat ctc cgc ttc ctg gac atg agc cag aac cag	1184
Ser Ser Asp Leu Ala Asp Leu Arg Phe Leu Asp Met Ser Gln Asn Gln	
325 330 335	
ttc cag tac ctg cca gac ggc ttc ctg agg aaa atg cct tcc ctc tcc	1232
Phe Gln Tyr Leu Pro Asp Gly Phe Leu Arg Lys Met Pro Ser Leu Ser	
340 345 350 355	
cac ctg aac ctc cac cag aat tgc ctg atg acg ctt cac att cgg gag	1280
His Leu Asn Leu His Gln Asn Cys Leu Met Thr Leu His Ile Arg Glu	
360 365 370	
cac gag ccc ccc gga gcg ctc acc gag ctg gac ctg agc cac aac cag	1328
His Glu Pro Pro Gly Ala Leu Thr Glu Leu Asp Leu Ser His Asn Gln	
375 380 385	
ctg tcg gag ctg cac ctg gct ccg ggg ctg gcc agc tgc ctg ggc agc	1376
Leu Ser Glu Leu His Leu Ala Pro Gly Leu Ala Ser Cys Leu Gly Ser	
390 395 400	
ctg cgc ttg ttc aac ctg agc tcc aac cag ctc ctg ggc gtc ccc cct	1424

004260" T E E L 092700

Leu Arg Leu Phe Asn Leu Ser Ser Asn Gln Leu Leu Gly Val Pro Pro	
405 410 415	
ggc ctc ttc gcc aat gct agg aac atc act aca ctt gac atg agc cac	1472
Gly Leu Phe Ala Asn Ala Arg Asn Ile Thr Thr Leu Asp Met Ser His	
420 425 430 435	
aat cag atc tca ctt tgt ccc ctg cca gct gcc tcg gac cgg gtg ggc	1520
Asn Gln Ile Ser Leu Cys Pro Leu Pro Ala Ala Ser Asp Arg Val Gly	
440 445 450	
ccc cct agc tgt gtg gat ttc agg aat atg gca tct tta agg agc ctg	1568
Pro Pro Ser Cys Val Asp Phe Arg Asn Met Ala Ser Leu Arg Ser Leu	
455 460 465	
tct ctg gag ggc tgt ggc ctg ggg gca ttg cca gac tgc cca ttc caa	1616
Ser Leu Glu Gly Cys Gly Leu Gly Ala Leu Pro Asp Cys Pro Phe Gln	
470 475 480	
ggg acc tcc ctg acc tac tta gac ctc tca agc aac tgg ggg gtt ctg	1664
Gly Thr Ser Leu Thr Tyr Leu Asp Leu Ser Ser Asn Trp Gly Val Leu	
485 490 495	
aat ggg agc ctc gcc cca ctc cag gat gtt gcc ccc atg tta cag gtc	1712
Asn Gly Ser Leu Ala Pro Leu Gln Asp Val Ala Pro Met Leu Gln Val	
500 505 510 515	
ctg tct ctc agg aac atg ggc ctc cac tcc agc ttt atg gcg ttg gac	1760
Leu Ser Leu Arg Asn Met Gly Leu His Ser Ser Phe Met Ala Leu Asp	
520 525 530	
ttc tct ggg ttt ggg aat ctc agg gac tta gat ctg tcg ggg aat tgc	1808
Phe Ser Gly Phe Gly Asn Leu Arg Asp Leu Asp Leu Ser Gly Asn Cys	
535 540 545	
ttg ccc atc ttc cca agg ttt ggg ggc agc ctg gcc ctg gag acc ctg	1856
Leu Pro Ile Phe Pro Arg Phe Gly Gly Ser Leu Ala Leu Glu Thr Leu	
550 555 560	
gat ctc cgt aga aac tcg ctc aca gcc ctt ccc cag aag gct gtg tct	1904
Asp Leu Arg Arg Asn Ser Leu Thr Ala Leu Pro Gln Lys Ala Val Ser	
565 570 575	
gag cag ctc tcg aga ggt ctg cgg acc atc tac ctc agt cag aat cca	1952
Glu Gln Leu Ser Arg Gly Leu Arg Thr Ile Tyr Leu Ser Gln Asn Pro	
580 585 590 595	
tat gac tgc tgt ggg gtg gat ggc tgg ggg gcc ctg cag cat ggg cag	2000
Tyr Asp Cys Cys Gly Val Asp Gly Trp Gly Ala Leu Gln His Gly Gln	
600 605 610	
acg gtg gcc gac tgg gcc atg gtc acc tgc aac ctc tcc tcc aag atc	2048
Thr Val Ala Asp Trp Ala Met Val Thr Cys Asn Leu Ser Ser Lys Ile	
615 620 625	
atc cgc gtg acg gag ctg ccc gga ggt gtg cct cgg gac tgc aag tgg	2096
Ile Arg Val Thr Glu Leu Pro Gly Gly Val Pro Arg Asp Cys Lys Trp	
630 635 640	
gag cgg ctg gac ctg ggc ctg ctc tac ctc gtg ctc atc ctc ccc agc	2144

002260" T 2260" 002260"

Glu Arg Leu Asp Leu Gly Leu Leu Tyr Leu Val Leu Ile Leu Pro Ser
645 650 655

tgc ctc acc ctg ctg gtg gcc tgc act gtc atc gtc ctc act ttt aag 2192
Cys Leu Thr Leu Leu Val Ala Cys Thr Val Ile Val Leu Thr Phe Lys
660 665 670 675

aag cct ctg ctt cag gtc atc aag agc cgc tgc cac tgg tcc tcc gtt 2240
Lys Pro Leu Leu Gln Val Ile Lys Ser Arg Cys His Trp Ser Ser Val
680 685 690

tac tga cctggctgtg tgccaagact cgaaattcgg tccgcacaca acaggacact 2296
Tyr

ttctctgccca gctttcaaga tgtgatgcag aggccaagtc tgacgaattg aagtttcaat 2356
taaaatctaa tatgtttcca taactcatct gccacacca cgcattgtatt cggccgctct 2416
agaggatcct tgcctaagtc ga 2438

<210> 4
<211> 692
<212> PRT
<213> Homo sapiens

<400> 4

Met Glu Leu Leu Pro Leu Trp Leu Cys Leu Gly Phe His Phe Leu Thr
1 5 10 15

Val Gly Trp Arg Asn Arg Ser Gly Thr Ala Thr Ala Ala Ser Gln Gly
20 25 30

Val Cys Lys Leu Val Gly Gly Ala Ala Asp Cys Arg Gly Gln Ser Leu
35 40 45

Ala Ser Val Pro Ser Ser Leu Pro Pro His Ala Arg Met Leu Thr Leu
50 55 60

Asp Ala Asn Pro Leu Lys Thr Leu Trp Asn His Ser Leu Gln Pro Tyr
65 70 75 80

Pro Leu Leu Glu Ser Leu Ser Leu His Ser Cys His Leu Glu Arg Ile
85 90 95

Ser Arg Gly Ala Phe Gln Glu Gln Gly His Leu Arg Ser Leu Val Leu
100 105 110

Gly Asp Asn Cys Leu Ser Glu Asn Tyr Glu Glu Thr Ala Ala Ala Leu
115 120 125

His Ala Leu Pro Gly Leu Arg Arg Leu Asp Leu Ser Gly Asn Ala Leu
130 135 140

Thr Glu Asp Met Ala Ala Leu Met Leu Gln Asn Leu Ser Ser Leu Arg
145 150 155 160

Ser Val Ser Leu Ala Gly Asn Thr Ile Met Arg Leu Asp Asp Ser Val
165 170 175

Phe Glu Gly Leu Glu Arg Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr
180 185 190

Ile Phe Glu Ile Glu Gly Gly Ala Phe Asp Gly Leu Ala Glu Leu Arg
195 200 205

His Leu Asn Leu Ala Phe Asn Asn Leu Pro Cys Ile Val Asp Phe Gly
210 215 220

Leu Thr Arg Leu Arg Val Leu Asn Val Ser Tyr Asn Val Leu Glu Trp
225 230 235 240

Phe Leu Ala Thr Gly Gly Glu Ala Ala Phe Glu Leu Glu Thr Leu Asp
245 250 255

Leu Ser His Asn Gln Leu Leu Phe Phe Pro Leu Leu Pro Gln Tyr Ser
260 265 270

Lys Leu Arg Thr Leu Leu Leu Arg Asp Asn Asn Met Gly Phe Tyr Arg
275 280 285

Asp Leu Tyr Asn Thr Ser Ser Pro Arg Glu Met Val Ala Gln Phe Leu
290 295 300

Leu Val Asp Gly Asn Val Thr Asn Ile Thr Thr Val Ser Leu Trp Glu
305 310 315 320

Glu Phe Ser Ser Ser Asp Leu Ala Asp Leu Arg Phe Leu Asp Met Ser
325 330 335

Gln Asn Gln Phe Gln Tyr Leu Pro Asp Gly Phe Leu Arg Lys Met Pro
340 345 350

Ser Leu Ser His Leu Asn Leu His Gln Asn Cys Leu Met Thr Leu His
355 360 365

[illegible]

His Gly Gln Thr Val Ala Asp Trp Ala Met Val Thr Cys Asn Leu Ser
610 615 620

Ser Lys Ile Ile Arg Val Thr Glu Leu Pro Gly Gly Val Pro Arg Asp
625 630 635 640

Cys Lys Trp Glu Arg Leu Asp Leu Gly Leu Leu Tyr Leu Val Leu Ile
645 650 655

Leu Pro Ser Cys Leu Thr Leu Leu Val Ala Cys Thr Val Ile Val Leu
660 665 670

Thr Phe Lys Lys Pro Leu Leu Gln Val Ile Lys Ser Arg Cys His Trp
675 680 685

Ser Ser Val Tyr
690

<210> 5
<211> 2079
<212> DNA
<213> Homo sapiens

<400> 5
atggagttgc tgcctctttg gctctgectg ggttttcact tcttgaccgt gggctggagg 60
aacagaagcg gaacagccac agcagcctcc caaggagtct gcaagttggt ggggtggagcc 120
gctgactgcc gagggcagag cctcgcttcg gtgccagca gcctcccgcc ccacgcccgg 180
atgctcacc tggatgcaa ccctctcaag accctgtgga atcactccct ccagccttac 240
cctctcctgg agagcctcag cctgcacagc tgccacctgg agcgcacag ccgcggcgcc 300
ttccaggagc aaggtcacct gcgcagcctg gtcctggggg acaactgcct ctcagagaac 360
tacgaagaga cggcagccgc cctccacgcc ctgccggggc tgcggaggct ggacttgtca 420
ggaaacgccc tgacggagga catggcagcg ctcatgctcc agaactctc ctcgctgcgg 480
tccgtgtccc tggcggggaa caccatcatg cggctggacg actccgtctt cgagggcctg 540
gagcgtctcc gggagctgga tctgcagagg aactacatct tcgagatcga gggcggcgct 600
ttcgacggcc tggctgagct gaggcacctc aacctggcct tcaacaacct cccctgcatc 660
gtggacttcg ggctcacgcg gctgcgggtc ctcaacgtca gctacaacgt cctggagtgg 720
ttcctcgcga ccgggggaga ggctgccttc gagctggaga cgctggacct gtctcacaac 780
cagctgctgt tcttcccgtc gctgccccag tacagcaagt tgcggaccct cctgctgcgc 840
gacaacaaca tgggcttcta ccgggacctg tacaacacct cgctgccgag ggagatgggtg 900

0042360-092700

gcccagttcc tctctgtgga cggcaacgtg accaacaatca ccaccgtcag cctctgggaa 960
gaattctcct ccagcgacct cgcagatctc cgcttctctg acatgagcca gaaccagttc 1020
cagtacctgc cagacggctt cctgaggaaa atgccttccc tctcccacct gaacctccac 1080
cagaattgcc tgatgacgct tcacattcgg gagcacgagc cccccggagc gctcaccgag 1140
ctggacctga gccacaacca gctgtcggag ctgcacctgg ctccgggggt ggccagctgc 1200
ctgggcagcc tgcgcttggt caacctgagc tccaaccagc tctggggcgt ccccccctggc 1260
ctcttcgcca atgctaggaa catcaactaca cttgacatga gccacaatca gatctcactt 1320
tgtccccctgc cagctgcctc ggaccgggtg ggcccccccta gctgtgtgga tttcaggaat 1380
atggcatctt taaggagcct gtctctggag ggctgtggcc tgggggcatt gccagactgc 1440
ccattccaag ggacctccct gacctactta gacctctcaa gcaactgggg ggttctgaat 1500
gggagcctcg ccccaactcca ggatgttgcc cccatgttac aggtcctgtc tctcaggaac 1560
atgggcctcc actccagctt tatggcgttg gacttctctg ggtttgggaa tctcagggac 1620
ttagatctgt cggggaattg cttgcccatc ttcccaaggt ttgggggcag cctggccctg 1680
gagaccttg atctccgtag aaactcgctc acagcccttc ccagaaggc tgtgtctgag 1740
cagctctcga gaggtctgag gaccatctac ctcaagtcaga atccatatga ctgctgtggg 1800
gtggatggct ggggggacct gcagcatggg cagacgggtg ccgactgggc catggtcacc 1860
tgcaacctct cctccaagat catccgctg acggagctgc ccggagggtg gcctcgggac 1920
tgcaagtggg agcggctgga cctgggcctg ctctacctcg tgctcactc cccagctgc 1980
ctcacctgc tgggtggcctg cactgtcatc gtctcactt ttaagaagcc tctgcttcag 2040
gtcatcaaga gccgctgcca ctggctctcc gtttactga 2079

<210> 6
<211> 14
<212> PRT
<213> Homo sapiens

<400> 6

Leu Thr Glu Leu Asp Leu Ser His Asn Gln Leu Ser Glu Leu
1 5 10

<210> 7
<211> 14
<212> PRT
<213> Homo sapiens

<400> 7

Leu Arg Arg Leu Asp Leu Ser Gly Asn Ala Leu Thr Glu Asp

1 5 10

<210> 8
<211> 14
<212> PRT
<213> Homo sapiens

<400> 8

Phe Gly Asn Leu Arg Asp Leu Asp Leu Ser Gly Asn Cys Leu
1 5 10

<210> 9
<211> 14
<212> PRT
<213> Homo sapiens

<400> 9

Pro Gly Ala Leu Thr Glu Leu Asp Leu Ser His Asn Gln Leu
1 5 10

<210> 10
<211> 14
<212> PRT
<213> Homo sapiens

<400> 10

Leu Glu Thr Leu Asp Leu Ser His Asn Gln Leu Leu Phe Phe
1 5 10

<210> 11
<211> 14
<212> PRT
<213> Homo sapiens

<400> 11

Leu Thr Arg Leu Arg Val Leu Asn Val Ser Tyr Asn Val Leu
1 5 10

<210> 12
<211> 14
<212> PRT
<213> Homo sapiens

<400> 12

Leu Glu Thr Leu Asp Leu Arg Arg Asn Ser Leu Thr Ala Leu
1 5 10

<210> 13
<211> 14
<212> PRT
<213> Homo sapiens

<400> 13

Met Pro Ser Leu Ser His Leu Asn Leu His Gln Asn Cys Leu

1 5 10

<210> 14
<211> 14
<212> PRT
<213> Homo sapiens

<400> 14

Leu Glu Arg Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr Ile
1 5 10

<210> 15
<211> 18
<212> PRT
<213> Homo sapiens

<400> 15

Met Glu Leu Leu Pro Leu Trp Leu Cys Leu Gly Phe His Phe Leu Thr
1 5 10 15

Val Gly

<210> 16
<211> 26
<212> PRT
<213> Homo sapiens

<400> 16

Leu Gly Leu Leu Tyr Leu Val Leu Ile Leu Pro Ser Cys Leu Thr Leu
1 5 10 15

Leu Val Ala Cys Thr Val Ile Val Leu Thr
20 25

<210> 17
<211> 674
<212> PRT
<213> Homo sapiens

<400> 17

Trp Arg Asn Arg Ser Gly Thr Ala Thr Ala Ala Ser Gln Gly Val Cys
1 5 10 15

Lys Leu Val Gly Gly Ala Ala Asp Cys Arg Gly Gln Ser Leu Ala Ser
20 25 30

Val Pro Ser Ser Leu Pro Pro His Ala Arg Met Leu Thr Leu Asp Ala
35 40 45

Asn Pro Leu Lys Thr Leu Trp Asn His Ser Leu Gln Pro Tyr Pro Leu
50 55 60

Leu Glu Ser Leu Ser Leu His Ser Cys His Leu Glu Arg Ile Ser Arg
65 70 75 80

00672331-092700

Gly Ala Phe Gln Glu Gln Gly His Leu Arg Ser Leu Val Leu Gly Asp
85 90 95

Asn Cys Leu Ser Glu Asn Tyr Glu Glu Thr Ala Ala Ala Leu His Ala
100 105 110

Leu Pro Gly Leu Arg Arg Leu Asp Leu Ser Gly Asn Ala Leu Thr Glu
115 120 125

Asp Met Ala Ala Leu Met Leu Gln Asn Leu Ser Ser Leu Arg Ser Val
130 135 140

Ser Leu Ala Gly Asn Thr Ile Met Arg Leu Asp Asp Ser Val Phe Glu
145 150 155 160

Gly Leu Glu Arg Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr Ile Phe
165 170 175

Glu Ile Glu Gly Gly Ala Phe Asp Gly Leu Ala Glu Leu Arg His Leu
180 185 190

Asn Leu Ala Phe Asn Asn Leu Pro Cys Ile Val Asp Phe Gly Leu Thr
195 200 205

Arg Leu Arg Val Leu Asn Val Ser Tyr Asn Val Leu Glu Trp Phe Leu
210 215 220

Ala Thr Gly Gly Glu Ala Ala Phe Glu Leu Glu Thr Leu Asp Leu Ser
225 230 235 240

His Asn Gln Leu Leu Phe Phe Pro Leu Leu Pro Gln Tyr Ser Lys Leu
245 250 255

Arg Thr Leu Leu Leu Arg Asp Asn Asn Met Gly Phe Tyr Arg Asp Leu
260 265 270

Tyr Asn Thr Ser Ser Pro Arg Glu Met Val Ala Gln Phe Leu Leu Val
275 280 285

Asp Gly Asn Val Thr Asn Ile Thr Thr Val Ser Leu Trp Glu Glu Phe
290 295 300

Ser Ser Ser Asp Leu Ala Asp Leu Arg Phe Leu Asp Met Ser Gln Asn
305 310 315 320

Gln Phe Gln Tyr Leu Pro Asp Gly Phe Leu Arg Lys Met Pro Ser Leu
325 330 335

Ser His Leu Asn Leu His Gln Asn Cys Leu Met Thr Leu His Ile Arg
340 345 350

Glu His Glu Pro Pro Gly Ala Leu Thr Glu Leu Asp Leu Ser His Asn
355 360 365

Gln Leu Ser Glu Leu His Leu Ala Pro Gly Leu Ala Ser Cys Leu Gly
370 375 380

Ser Leu Arg Leu Phe Asn Leu Ser Ser Asn Gln Leu Leu Gly Val Pro
385 390 395 400

Pro Gly Leu Phe Ala Asn Ala Arg Asn Ile Thr Thr Leu Asp Met Ser
 405 410 415
 His Asn Gln Ile Ser Leu Cys Pro Leu Pro Ala Ala Ser Asp Arg Val
 420 425 430
 Gly Pro Pro Ser Cys Val Asp Phe Arg Asn Met Ala Ser Leu Arg Ser
 435 440 445
 Leu Ser Leu Glu Gly Cys Gly Leu Gly Ala Leu Pro Asp Cys Pro Phe
 450 455 460
 Gln Gly Thr Ser Leu Thr Tyr Leu Asp Leu Ser Ser Asn Trp Gly Val
 465 470 475 480
 Leu Asn Gly Ser Leu Ala Pro Leu Gln Asp Val Ala Pro Met Leu Gln
 485 490 495
 Val Leu Ser Leu Arg Asn Met Gly Leu His Ser Ser Phe Met Ala Leu
 500 505 510
 Asp Phe Ser Gly Phe Gly Asn Leu Arg Asp Leu Asp Leu Ser Gly Asn
 515 520 525
 Cys Leu Pro Ile Phe Pro Arg Phe Gly Gly Ser Leu Ala Leu Glu Thr
 530 535 540
 Leu Asp Leu Arg Arg Asn Ser Leu Thr Ala Leu Pro Gln Lys Ala Val
 545 550 555 560
 Ser Glu Gln Leu Ser Arg Gly Leu Arg Thr Ile Tyr Leu Ser Gln Asn
 565 570 575
 Pro Tyr Asp Cys Cys Gly Val Asp Gly Trp Gly Ala Leu Gln His Gly
 580 585 590
 Gln Thr Val Ala Asp Trp Ala Met Val Thr Cys Asn Leu Ser Ser Lys
 595 600 605
 Ile Ile Arg Val Thr Glu Leu Pro Gly Gly Val Pro Arg Asp Cys Lys
 610 615 620
 Trp Glu Arg Leu Asp Leu Gly Leu Leu Tyr Leu Val Leu Ile Leu Pro
 625 630 635 640
 Ser Cys Leu Thr Leu Leu Val Ala Cys Thr Val Ile Val Leu Thr Phe
 645 650 655
 Lys Lys Pro Leu Leu Gln Val Ile Lys Ser Arg Cys His Trp Ser Ser
 660 665 670
 Val Tyr

<210> 18
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 18

Val Ser Leu Ala Gly Asn Thr Ile Met Arg Leu Asp Asp Ser Val Phe
1 5 10 15

Glu Gly Leu Glu Arg Leu Arg Glu Leu Asp Leu Gln Arg Asn Tyr Ile
20 25 30

Phe Glu Ile Glu Gly Gly Ala Phe Asp Gly Leu Ala Glu Leu Arg His
35 40 45

Leu Asn Leu Ala Phe Asn Asn Leu Pro Cys Ile Val Asp Phe Gly Leu
50 55 60

Thr Arg Leu Arg Val Leu Asn Val Ser Tyr Asn Val Leu Glu Trp Phe
65 70 75 80

Leu Ala Thr Gly Gly Glu Ala Ala Phe Glu Leu Glu Thr Leu Asp Leu
85 90 95

Ser His Asn Gln Leu Leu Phe Phe Pro Leu Leu Pro Gln Tyr Ser Lys
100 105 110

Leu Arg Thr Leu Leu Leu Arg Asp Asn
115 120

<210> 19

<211> 626

<212> PRT

<213> Homo sapiens

<400> 19

Cys Lys Met Val Asp Lys Lys Val Ser Cys Gln Val Leu Gly Leu Leu
1 5 10 15

Gln Val Pro Ser Val Leu Pro Pro Asp Thr Glu Thr Leu Asp Leu Ser
20 25 30

Gly Asn Gln Leu Arg Ser Ile Leu Ala Ser Pro Leu Gly Phe Tyr Thr
35 40 45

Ala Leu Arg His Leu Asp Leu Ser Thr Asn Glu Ile Ser Phe Leu Gln
50 55 60

Pro Gly Ala Phe Gln Ala Leu Thr His Leu Glu His Leu Ser Leu Ala
65 70 75 80

His Asn Arg Leu Ala Met Ala Thr Ala Leu Ser Ala Gly Gly Leu Gly
85 90 95

Pro Leu Pro Arg Val Thr Ser Leu Asp Leu Ser Gly Asn Ser Leu Tyr
100 105 110

Ser Gly Leu Leu Glu Arg Leu Leu Gly Glu Ala Pro Ser Leu His Thr
115 120 125

Leu Ser Leu Ala Glu Asn Ser Leu Thr Arg Leu Thr Arg His Thr Phe
130 135 140

Arg Asp Met Pro Ala Leu Glu Gln Leu Asp Leu His Ser Asn Val Leu

145 150 155 160
 Met Asp Ile Glu Asp Gly Ala Phe Glu Gly Leu Pro Arg Leu Thr His
 165 170 175
 Leu Asn Leu Ser Arg Asn Ser Leu Thr Cys Ile Ser Asp Phe Ser Leu
 180 185 190
 Gln Gln Leu Arg Val Leu Asp Leu Ser Cys Asn Ser Ile Glu Ala Phe
 195 200 205
 Gln Thr Ala Ser Gln Pro Gln Ala Glu Phe Gln Leu Thr Trp Leu Asp
 210 215 220
 Leu Arg Glu Asn Lys Leu Leu His Phe Pro Asp Leu Ala Ala Leu Pro
 225 230 235 240
 Arg Leu Ile Tyr Leu Asn Leu Ser Asn Asn Leu Ile Arg Leu Pro Thr
 245 250 255
 Gly Pro Pro Gln Asp Ser Lys Gly Ile His Ala Pro Ser Glu Gly Trp
 260 265 270
 Ser Ala Leu Pro Leu Ser Ala Pro Ser Gly Asn Ala Ser Gly Arg Pro
 275 280 285
 Leu Ser Gln Leu Leu Asn Leu Asp Leu Ser Tyr Asn Glu Ile Glu Leu
 290 295 300
 Ile Pro Asp Ser Phe Leu Glu His Leu Thr Ser Leu Cys Phe Leu Asn
 305 310 315 320
 Leu Ser Arg Asn Cys Leu Arg Thr Phe Glu Ala Arg Arg Leu Gly Ser
 325 330 335
 Leu Pro Cys Leu Met Leu Leu Asp Leu Ser His Asn Ala Leu Glu Thr
 340 345 350
 Leu Glu Leu Gly Ala Arg Ala Leu Gly Ser Leu Arg Thr Leu Leu Leu
 355 360 365
 Gln Gly Asn Ala Leu Arg Asp Leu Pro Pro Tyr Thr Phe Ala Asn Leu
 370 375 380
 Ala Ser Leu Gln Arg Leu Asn Leu Gln Gly Asn Arg Val Ser Pro Cys
 385 390 395 400
 Gly Gly Pro Asp Glu Pro Gly Pro Ser Gly Cys Val Ala Phe Ser Gly
 405 410 415
 Ile Thr Ser Leu Arg Ser Leu Ser Leu Val Asp Asn Glu Ile Glu Leu
 420 425 430
 Leu Arg Ala Gly Ala Phe Leu His Thr Pro Leu Thr Glu Leu Asp Leu
 435 440 445
 Ser Ser Asn Pro Gly Leu Glu Val Ala Thr Gly Ala Leu Gly Gly Leu
 450 455 460
 Glu Ala Ser Leu Glu Val Leu Ala Leu Gln Gly Asn Gly Leu Met Val

465 470 475 480
 Leu Gln Val Asp Leu Pro Cys Phe Ile Cys Leu Lys Arg Leu Asn Leu
 485 490 495
 Ala Glu Asn Arg Leu Ser His Leu Pro Ala Trp Thr Gln Ala Val Ser
 500 505 510
 Leu Glu Val Leu Asp Leu Arg Asn Asn Ser Phe Ser Leu Leu Pro Gly
 515 520 525
 Ser Ala Met Gly Gly Leu Glu Thr Ser Leu Arg Arg Leu Tyr Leu Gln
 530 535 540
 Gly Asn Pro Leu Ser Cys Cys Gly Asn Gly Trp Leu Ala Ala Gln Leu
 545 550 555 560
 His Gln Gly Arg Val Asp Val Asp Ala Thr Gln Asp Leu Ile Cys Arg
 565 570 575
 Phe Ser Ser Gln Glu Glu Val Ser Leu Ser His Val Arg Pro Glu Asp
 580 585 590
 Cys Glu Lys Gly Gly Leu Lys Asn Ile Asn Leu Ile Ile Ile Leu Thr
 595 600 605
 Phe Ile Leu Val Ser Ala Ile Leu Leu Thr Thr Leu Ala Ala Cys Cys
 610 615 620
 Cys Val
 625
 <210> 20
 <211> 510
 <212> PRT
 <213> Baboon
 <400> 20
 Pro Arg Ser Leu Glu Gly Ala Glu Pro Gly Thr Pro Gly Glu Ala Glu
 5 10 15
 Gly Pro Ala Cys Pro Ala Thr Cys Ala Cys Ser Tyr Asp Asp Glu Val
 20 25 30
 Asn Glu Leu Ser Val Phe Cys Ser Ser Arg Asn Leu Thr Arg Leu Pro
 35 40 45
 Asp Gly Ile Pro Gly Gly Thr Gln Ala Leu Trp Leu Asp Ser Asn Asn
 50 55 60
 Leu Ser Ser Ile Pro Pro Ala Ala Phe Arg Asn Leu Ser Ser Leu Ala
 65 70 75 80
 Phe Leu Asn Leu Gln Gly Gly Gln Leu Gly Ser Leu Glu Pro Gln Ala
 85 90 95
 Leu Leu Gly Leu Glu Asn Leu Cys His Leu His Leu Glu Arg Asn Gln
 100 105 110

Leu Arg Ser Leu Ala Val Gly Thr Phe Ala Tyr Thr Pro Ala Leu Ala
115 120 125

Leu Leu Gly Leu Ser Asn Asn Arg Leu Ser Arg Leu Glu Asp Gly Leu
130 135 140

Phe Glu Gly Leu Gly Asn Leu Trp Asp Leu Asn Leu Gly Trp Asn Ser
145 150 155 160

Leu Ala Val Leu Pro Asp Ala Ala Phe Arg Gly Leu Gly Gly Leu Arg
165 170 175

Glu Leu Val Leu Ala Gly Asn Arg Leu Ala Tyr Leu Gln Pro Ala Leu
180 185 190

Phe Ser Gly Leu Ala Glu Leu Arg Glu Leu Asp Leu Ser Arg Asn Ala
195 200 205

Leu Arg Ala Ile Lys Ala Asn Val Phe Ala Gln Leu Pro Arg Leu Gln
210 215 220

Lys Leu Tyr Leu Asp Arg Asn Leu Ile Ala Ala Val Ala Pro Gly Ala
225 230 235 240

Phe Leu Gly Leu Lys Ala Leu Arg Trp Leu Asp Leu Ser His Asn Arg
245 250 255

Val Ala Gly Leu Leu Glu Asp Thr Phe Pro Gly Leu Leu Gly Leu Arg
260 265 270

Val Leu Arg Leu Ser His Asn Ala Ile Ala Ser Leu Arg Pro Arg Thr
275 280 285

Phe Glu Asp Leu His Phe Leu Glu Glu Leu Gln Leu Gly His Asn Arg
290 295 300

Ile Arg Gln Leu Ala Glu Arg Ser Phe Glu Gly Leu Gly Gln Leu Glu
305 310 315 320

Val Leu Thr Leu Asp His Asn Gln Leu Gln Glu Val Lys Val Gly Ala
325 330 335

Phe Leu Gly Leu Thr Asn Val Ala Val Met Asn Leu Ser Gly Asn Cys
340 345 350

Leu Arg Asn Leu Pro Glu Gln Val Phe Arg Gly Leu Gly Lys Leu His
355 360 365

Ser Leu His Leu Glu Gly Ser Cys Leu Gly Arg Ile Arg Pro His Thr
370 375 380

Phe Ala Gly Leu Ser Gly Leu Arg Arg Leu Phe Leu Lys Asp Asn Gly
385 390 395 400

Leu Val Gly Ile Glu Glu Gln Ser Leu Trp Gly Leu Ala Glu Leu Leu
405 410 415

Glu Leu Asp Leu Thr Ser Asn Gln Leu Thr His Leu Pro His Gln Leu
420 425 430

Phe Gln Gly Leu Gly Lys Leu Glu Tyr Leu Leu Leu Ser His Asn Arg
 435 440 445

Leu Ala Glu Leu Pro Ala Asp Ala Leu Gly Pro Leu Gln Arg Ala Phe
 450 455 460

Trp Leu Asp Val Ser His Asn Arg Leu Glu Ala Leu Pro Gly Ser Leu
 465 470 475 480

Leu Ala Ser Leu Gly Arg Leu Arg Tyr Leu Asn Leu Arg Asn Asn Ser
 485 490 495

Leu Arg Thr Phe Thr Pro Gln Pro Pro Gly Leu Glu Arg Leu
 500 505 510

<210> 21
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 21

Gly Met Thr Val Leu Gln Arg Leu Met Ile Ser Asp Ser His Ile Ser
 1 5 10 15

Ala Val Ala Pro Gly Thr Phe Ser Asp Leu Ile Lys Leu Lys Thr Leu
 20 25 30

Arg Leu Ser Arg Asn Lys Ile Thr His Leu Pro Gly Ala Leu Leu Asp
 35 40 45

Lys Met Val Leu Leu Glu Gln Leu Phe Leu Asp His Asn Ala Leu Arg
 50 55 60

Gly Ile Asp Gln Asn Met Phe Gln Lys Leu Val Asn Leu Gln Glu Leu
 65 70 75 80

Ala Leu Asn Gln Asn Gln Leu Asp Phe Leu Pro Ala Ser Leu Phe Thr
 85 90 95

Asn Leu Glu Asn Leu Lys Leu Leu Asp Leu Ser Gly Asn Asn Leu Thr
 100 105 110

His Leu Pro Lys Gly Leu Leu Gly Ala Gln Ala Lys Leu Glu Arg Leu
 115 120 125

Leu Leu His Ser Asn Arg Leu Val Ser Leu Asp Ser Gly Leu Leu Asn
 130 135 140

Ser Leu Gly Ala Leu Thr Glu Leu Gln Phe His Arg Asn His Ile Arg
 145 150 155 160

Ser Ile Ala Pro Gly Ala Phe Asp Arg Leu Pro Asn Leu Ser Ser Leu
 165 170 175

Thr Leu Ser Arg Asn His Leu Ala Phe Leu Pro Ser Ala Leu Phe Leu
 180 185 190

His Ser His Asn Leu Thr Leu Leu Thr Leu Phe Glu Asn Pro Leu Ala
 195 200 205

002260 "T227960

Glu Leu Pro Gly Val Leu Phe Gly Glu Met Gly Gly Leu Gln Glu Leu
210 215 220

Trp Leu Asn Arg Thr Gln Leu Arg Thr Leu Pro Ala Ala Ala Phe Arg
225 230 235 240

Asn Leu Ser Arg Leu Arg Tyr Leu Gly Val Thr Leu Ser Pro Arg Leu
245 250 255

Ser Ala Leu Pro Gln Gly Ala Phe Gln Gly Leu Gly Glu Leu Gln Val
260 265 270

Leu Ala Leu His Ser Asn Gly Leu Thr Ala Leu Pro Asp Gly Leu Leu
275 280 285

Arg Gly Leu Gly Lys Leu Arg Gln Val Ser Leu Arg Arg Asn Arg Leu
290 295 300

Arg Ala Leu Pro Arg Ala Leu Phe Arg Asn Leu Ser Ser Leu Glu Ser
305 310 315 320

Val Gln Leu Asp His Asn Gln Leu Glu Thr Leu Pro Gly Asp Val Phe
325 330 335

Gly Ala Leu Pro Arg Leu Thr Glu Val Leu Leu Gly His Asn Ser Trp
340 345 350

Arg Cys Asp Cys Gly Leu Gly Pro Phe Leu Gly Trp Leu Arg Gln His
355 360 365

<210> 22

<211> 457

<212> PRT

<213> synthetic construct

<400> 22

Gly Thr Gln Ala Leu Trp Leu Asp Gly Asn Asn Leu Ser Ser Val Pro
1 5 10 15

Pro Ala Ala Phe Gln Asn Leu Ser Ser Leu Gly Phe Leu Asn Leu Gln
20 25 30

Gly Gly Gln Leu Gly Ser Leu Glu Pro Gln Ala Leu Leu Gly Leu Glu
35 40 45

Asn Leu Cys His Leu His Leu Glu Arg Asn Gln Leu Arg Ser Leu Ala
50 55 60

Leu Gly Thr Phe Ala His Thr Pro Ala Leu Ala Ser Leu Gly Leu Ser
65 70 75 80

Asn Asn Arg Leu Ser Arg Leu Glu Asp Gly Leu Phe Glu Gly Leu Gly
85 90 95

Ser Leu Trp Asp Leu Asn Leu Gly Trp Asn Ser Leu Ala Val Leu Pro
100 105 110

Asp Ala Ala Phe Arg Gly Leu Gly Ser Leu Arg Glu Leu Val Leu Ala

115

120

125

Gly Asn Arg Leu Ala Tyr Leu Gln Pro Ala Leu Phe Ser Gly Leu Ala
130 135 140

Glu Leu Arg Glu Leu Asp Leu Ser Arg Asn Ala Leu Arg Ala Ile Lys
145 150 155 160

Ala Asn Val Phe Val Gln Leu Pro Arg Leu Gln Lys Leu Tyr Leu Asp
165 170 175

Arg Asn Leu Ile Ala Ala Val Ala Pro Gly Ala Phe Leu Gly Leu Lys
180 185 190

Ala Leu Arg Trp Leu Asp Leu Ser His Asn Arg Val Ala Gly Leu Leu
195 200 205

Glu Asp Thr Phe Pro Gly Leu Leu Gly Leu Arg Val Leu Arg Leu Ser
210 215 220

His Asn Ala Ile Ala Ser Leu Arg Pro Arg Thr Phe Lys Asp Leu His
225 230 235 240

Phe Leu Glu Glu Leu Gln Leu Gly His Asn Arg Ile Arg Gln Leu Ala
245 250 255

Glu Arg Ser Phe Glu Gly Leu Gly Gln Leu Glu Val Leu Thr Leu Asp
260 265 270

His Asn Gln Leu Gln Glu Val Lys Ala Gly Ala Phe Leu Gly Leu Thr
275 280 285

Asn Val Ala Val Met Asn Leu Ser Gly Asn Cys Leu Arg Asn Leu Pro
290 295 300

Glu Gln Val Phe Arg Gly Leu Gly Lys Leu His Ser Leu His Leu Glu
305 310 315 320

Gly Ser Cys Leu Gly Arg Ile Arg Pro His Thr Phe Thr Gly Leu Ser
325 330 335

Gly Leu Arg Arg Leu Phe Leu Lys Asp Asn Gly Leu Val Gly Ile Glu
340 345 350

Glu Gln Ser Leu Trp Gly Leu Ala Glu Leu Leu Glu Leu Asp Leu Thr
355 360 365

Ser Asn Gln Leu Thr His Leu Pro His Arg Leu Phe Gln Gly Leu Gly
370 375 380

Lys Leu Glu Tyr Leu Leu Leu Ser Arg Asn Arg Leu Ala Glu Leu Pro
385 390 395 400

Ala Asp Ala Leu Gly Pro Leu Gln Arg Ala Phe Trp Leu Asp Val Ser
405 410 415

His Asn Arg Leu Glu Ala Leu Pro Asn Ser Leu Leu Ala Pro Leu Gly
420 425 430

Arg Leu Arg Tyr Leu Ser Leu Arg Asn Asn Ser Leu Arg Thr Phe Thr

435

440

445

Pro Gln Pro Pro Gly Leu Glu Arg Leu
450 455

09672221.092700